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09/812,350	03/20/2001	Susan Lindquist	HO-P01979US2	1595

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EXAMINER	
BAUM, STUART F	

ART UNIT	PAPER NUMBER
1638	

DATE MAILED: 03/24/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/812,350	LINDQUIST ET AL.	
	Examiner	Art Unit	
	Stuart F. Baum	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *06 January 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-16 and 27-44* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-16 and 27-44* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *20 March 2001* is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *7/3/2001*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

1. Claims 1-16, and 27-44 are pending.

2. Applicant's election with traverse of Group I, claims 1-16 and 27-28 including SEQ ID NO:17 encoding SEQ ID NO:30 filed 1/6/2004 is acknowledged. The traversal is on the ground(s) that it is unreasonable to require election of species, given that they are all closely related sequences of the Hsp100 family group and it would not be an undue burden to search more than one (page 7, 1st paragraph).

This is not found persuasive because the Examiner maintains that the USPTO policy is that individual sequences encoding different proteins are patentably distinct inventions, rather than species of a common genus.

The requirement is still deemed proper and is therefore made FINAL.

Claims 17-26 have been canceled.

Claims 29-44 have been newly added.

3. Claims 1-16 and 27-44 are examined in the present office action.

Specification

4. The attempt to incorporate subject matter into this application by reference to Schirmer et al (1994 Plant Cell 6:1899-1909, listed in IDS), is improper because Applicant relies on the Shirmer et al reference for essential material, i.e., the sequence of the Arabidopsis Hsp101 cDNA sequence (See page 49, paragraph 176 and page 61, paragraph 218 of the Application). It is believed that the DNA and amino acid sequence of Shirmer et al correspond to SEQ ID NO:30

encoding SEQ ID NO:17, but that is not explicitly stated in the application. A declaration stating as such will obviate the objection.

Claim Objections

5. Claims 2, 4 are objected to for reading on non-elected inventions. Correction is required.

Claim 30, 38, 39, line 2 is objected to for omitting the word "sequence" after the recitation "acid".

Claims 30 and 39, line 3, is objected to for inadvertently reciting "(c)" at the beginning of the line.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

6. Claims 1-16, and 29-44 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The rejection includes dependent claims.

In claim 1, the metes and bounds of "Hsp100 family amino acid sequence" have not been defined. Applicants define the family in term of amino acid homology at about at least 40% to Arabidopsis thaliana Hsp101 but then go on to describe an alternative embodiment directed to sequences having similarity to the yeast Hsp104 sequence (page 13 and 14, paragraph 58). As described below, both "homology" and "similarity" are also indefinite. Applicants do not

present further guidance which permits one skilled in the art to accurately discriminate between sequences that are encompassed by Applicants' recitation of "Hsp100 family amino acid sequence" and those sequences that are not encompassed. All subsequent recitations of "Hsp100 family amino acid sequence" are also rejected.

In claim 4, the metes and bounds of "sequence similarity" have not been defined. Applicant has not specified what constitutes "similar" when comparing nucleic acid sequences. Is guanine similar to adenine? The term "similarity" is generally reserved for amino acid sequence comparisons where there are conserved amino acids.

In claim 34, it is recommended that the word "homology" be replaced with --sequence identity--. Support for "sequence identity" can be found on page 15, paragraph 61. The meaning of the word "homology" is indefinite as it is not clear how relatedness is determined, whether by sequence relatedness alone, by evolutionary relatedness, or by some other means. Amino acid or nucleotide sequences cannot exhibit a particular "level of homology" (Reeck et al., 1987, Cell 50:667, left column, 2nd paragraph). All subsequent recitations of "homology" are also rejected.

Claim 34 is indefinite in the recitation "Arabidopsis Hsp101 amino acid sequence". The sole designation of an amino acid sequence by "Arabidopsis Hsp101" is arbitrary and creates ambiguity in the claims. For example, the amino acid sequence in this application could be designated by some other arbitrary means, or the assignment of said name could be arbitrarily changed to designate a different amino acid sequence. If either event occurs, one's ability to determine the metes and bounds of the claim would be impaired. See *In re Hammack*, 427 F .2d

1378, 1382; 166 USPQ 204, 208 (CCPA 1970). Amendment of the claim to refer to a specific SEQ ID NO would obviate this rejection.

In claim 37, the metes and bounds of "functionally equivalent" have not been defined. Applicants have not stated what the explicit function of an Hsp100 polypeptide is, nor have Applicants disclosed functions that are considered to be "functionally equivalent".

Written Description

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

7. Claims 1, 3-16, and 27-44 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The claims are broadly drawn to a transgenic plants, methods of increasing stress tolerance of a plant and method of producing a crop comprising any nucleic acid sequence encoding any plant Hsp100 family amino acid sequence, any nucleic acid sequence that has sequence similarity with SEQ ID NO:30, or any nucleic acid sequence encoding any amino acid sequence having at least about 60%, 70%, or 80% overall amino acid homology to Arabidopsis Hsp101 amino acid sequence, or a functional equivalent of an Arabidopsis Hsp101 amino acid sequence.

Applicants disclose SEQ ID NO:30 encoding SEQ ID NO:17.

The Applicants do not identify essential regions of a plant Hsp100 amino acid sequence, essential regions of the genus of plant Hsp100 family amino acid sequences, essential regions of

SEQ ID NO:30, nor essential regions of an Arabidopsis Hsp101 amino acid sequence or functional equivalent thereof. Applicants do not describe any nucleic acid sequence that encodes an amino acid sequence having at least about 60%, 70%, or 80% overall amino acid homology to Arabidopsis Hsp101 amino acid sequence and has the same function as an Arabidopsis Hsp101 amino acid sequence. The Federal Circuit has recently clarified the application of the written description requirement to inventions in the field of biotechnology. See University of California v. Eli Lilly and Co., 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). In summary, the court stated that a written description of an invention requires a precise definition, one that defines the structural features of the chemical genus that distinguishes it from other chemical structures. A definition by function does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is. The court goes on to say, "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." *See University of California v. Eli Lilly and Co.*, 119 F.3d 1559; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). Applicants fail to describe a representative number of polynucleotide sequences encoding an Arabidopsis Hsp101 protein or a plant Hsp100 protein falling within the scope of the claimed genus of polynucleotides that are encompassed by Applicants broad recitations including any plant Hsp100 family amino acid sequence, any nucleic acid sequence having sequence similarity with SEQ ID NO:30, or any nucleic acid sequence encoding an amino acid sequence having at least about 60%, 70%, or 80% overall amino acid homology to Arabidopsis Hsp101 amino acid sequence, or functional equivalent

thereof. Applicants only describe a single sequence of SEQ ID NO:30 encoding SEQ ID NO:17. Furthermore, Applicants fail to describe structural features common to members of the claimed genus of polynucleotides. Hence, Applicants fail to meet either prong of the two-prong test set forth by *Eli Lilly*. Furthermore, given the lack of description of the necessary elements essential for the Arabidopsis Hsp101 protein, or the plant Hsp100 family amino acid sequence, it remains unclear what features identify an Arabidopsis Hsp101 protein, or the plant Hsp100 family amino acid sequence. Since the genus of Arabidopsis Hsp101 protein, or the plant Hsp100 family amino acid sequence has not been described by specific structural features, the specification fails to provide an adequate written description to support the breath of the claims.

Sequences that are similar to SEQ ID NO:30, or sequences that are encompassed by the recitation a nucleic acid sequence encoding a plant Hsp100 family amino acid sequence, or sequences, or sequences that encode an amino acid sequence having at least about 60%, 70%, or 80% homology to an Arabidopsis Hsp101 amino acid sequence, or a functional equivalent thereof, encompass naturally occurring allelic variants, mutants of the stated proteins, as well as sequences encoding proteins having no known heat shock protein activity, of which Applicant is not in possession. Absent of such disclosure, one skilled in the art cannot determine the genus of sequences based upon the disclosure of the sequence of SEQ ID NO:30 encoding SEQ ID NO:17 with any certainty or predictability. Accordingly, the specification fails to provide an adequate written description to support the broad claims. (See Written Description guidelines published in Federal Register/Vol. 66, No.4/Friday, January 5, 2001/Notices: p.1099-1111).

Scope of Enablement

8. Claims 1, 3-16, and 29-44 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for transgenic plants, methods of increasing stress tolerance of a plant, and method of producing a crop comprising overexpressing a nucleic acid encoding the Arabidopsis Hsp101 of SEQ ID NO:17, does not reasonably provide enablement for claims broadly drawn to transgenic plants, methods of increasing stress tolerance of a plant, and method of producing a crop comprising overexpressing any nucleic acid sequence encoding any plant Hsp100 family amino acid sequence, any nucleic acid sequence that has sequence similarity with SEQ ID NO:30, any nucleic acid sequence encoding any amino acid sequence having at least about 60%, 70%, or 80% overall amino acid homology to Arabidopsis Hsp101 amino acid sequence, or any nucleic acid sequence encoding an amino acid sequence that is functionally equivalent to any Hsp100 amino acid sequence, wherein the nucleic acid sequence is operably linked to a constitutive or heat inducible promoter. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

The claimed invention is not supported by an enabling disclosure taking into account the *Wands* factors. *In re Wands,* 858/F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988). *In re Wands* lists a number of factors for determining whether or not undue experimentation would be required by one skilled in the art to make and/or use the invention. These factors are: the quantity of experimentation necessary, the amount of direction or guidance presented, the presence or absence of working examples of the invention, the nature of the invention, the state of the prior

art, the relative skill of those in the art, the predictability or unpredictability of the art, and the breadth of the claim.

The claims are broadly drawn to a any nucleic acid sequence encoding any plant Hsp100 family amino acid sequence, any nucleic acid sequence that has sequence similarity with SEQ ID NO:30, any nucleic acid sequence encoding any amino acid sequence having at least about 60%, 70%, or 80% overall amino acid homology to Arabidopsis Hsp101 amino acid sequence, or any nucleic acid sequence encoding an amino acid sequence that is functionally equivalent to any Hsp100 amino acid sequence, wherein the nucleic acid sequence is operably linked to a constitutive or heat inducible promoter.

Applicants disclose transforming Arabidopsis plants with a construct comprising the 35S CaMV promoter operably linked to the full length cDNA of Columbia Hsp101 (page 49, paragraph 176; page 61, paragraph 218), transformed into plants to yield plants that survive higher temperatures compared to plants not transformed with said construct (page 56, Table 2; page 58-59, paragraphs 212-213). The office is interpreting the cDNA of Columbia Hsp101 to be SEQ ID NO:30 encoding SEQ ID NO:17 because Applicant references Schimer et al (1994 Plant Cell 6:1899-1909, listed in IDS) whose DNA and protein sequence exhibit 100% sequence identity to said SEQ ID NO's.

Applicants fail to teach any nucleic acid sequence encoding any plant Hsp100 family amino acid sequence, any nucleic acid sequence that has sequence similarity with SEQ ID NO:30, any nucleic acid sequence encoding any amino acid sequence having at least about 60%, 70%, or 80% overall amino acid homology to Arabidopsis Hsp101 amino acid sequence, or any nucleic acid sequence encoding an amino acid sequence that is functionally equivalent to any

Hsp100 amino acid sequence, wherein the nucleic acid sequence is operably linked to a constitutive or heat inducible promoter and plants transformed therewith.

The state-of-the-art is such that one of skill in the art cannot predict which nucleic acids that exhibit sequence similarity with SEQ ID NO:30, or which nucleic acid sequence encoding any amino acid sequence having at least about 60%, 70%, or 80% overall amino acid homology to Arabidopsis Hsp101 amino acid sequence will encode a protein with the same activity as a protein encoded by SEQ ID NO:30. The prediction of protein structure from sequence data and, in turn, utilizing predicted structural determinations to ascertain functional aspects of the protein, is extremely complex, and the positions within the protein's sequence where amino acid substitutions can be made with a reasonable expectation of maintaining function are limited (Bowie et al, Science 247:1306-1310, 1990, see especially page 1306). Proteins may be sensitive to alterations in even a single amino acid in a sequence. For example, the replacement of a glycine residue located within the START domain of either the PHABULOSA or PHAVOLUTA protein receptor with either an alanine or aspartic acid residue, alters the sterol/lipid binding domain (McConnell et al, Nature 411 (6838):709-713, 2001, see especially page 710, left column, 2nd paragraph).

Applicants have not disclosed how one makes or isolates any of the sequences that are encompassed by Applicants' broad claims. Applicants have not taught which regions of the respective polynucleotides can be used to amplify any of said polynucleotides or which regions can be used as a probe to isolate any of said polynucleotide sequences.

The state-of-the-art teaches that transforming plants with heat shock proteins produces unpredictable results. Malik et al (1999 The Plant Journal 20(1):89-99) teach over-expression of

a chloroplast heat shock protein in Arabidopsis resulted in abundant expression of the protein, but no increase in thermotolerance (page 89, right column, 3rd paragraph). Heat shock proteins also have different endogenous functions. Schirmer et al (1996, TIBS 21, August, pages 289-296, listed in IDS) teach that the HSP100 protein from *Baccillus subtilis* are required for tolerance to high salt and HSP100 from *Pasteurella haemolytica* functions as an inhibitor of leukotoxin expression, for example (page 289, middle and end of 1st paragraph).

In the absence of guidance, undue trial and error experimentation would be required for one of ordinary skill in the art to screen through the multitude of non-exemplified sequences encompassed in Applicants' broad claims, either by using non-disclosed fragments of SEQ ID NO:30 as probes or by designing primers to undisclosed regions of SEQ ID NO:30 and isolating or amplifying fragments, subcloning the fragments, producing expression vectors and transforming plants therewith, in order to identify those, if any, that when over-expressed have increased thermotolerance of the transformed plant and encode any plant Hsp100 family amino acid sequence, or exhibit sequence similarity with SEQ ID NO:30, or encode any amino acid sequence having at least about 60%, 70%, or 80% overall amino acid homology to Arabidopsis Hsp101 amino acid sequence, or encodes an amino acid sequence that is functionally equivalent to any Hsp100 amino acid sequence.

Therefore, given the breadth of the claims; the lack of guidance and examples; the unpredictability in the art; and the state-of-the-art as discussed above, undue experimentation would be required to practice the claimed invention, and therefore the invention is not enabled.

Claim Rejections - 35 USC § 102

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

9. Claims 1, 3, 5, 7-9, 12-13, 27, and 29-32 are rejected under 35 U.S.C. 102(a) as being anticipated by Malik et al (1999 The Plant Journal 20(1):89-99).

The claims are drawn to a transgenic plant and method of increasing stress tolerance of a plant, wherein the stress is thermotolerance comprising a construct comprising a promoter operably linked to a nucleic acid sequence encoding a plant Hsp100 family amino acid sequence, wherein said plant Hsp100 family amino acid sequence is endogenous to said transgenic plant, and wherein said transgenic plant is a food plant, and wherein said promoter is the 35S cauliflower mosaic virus promoter, and wherein said amino acid sequence protects the plant from more than one type of stress and is necessary for cellular functioning when a stress is present and is not necessary for cellular functioning when the stress is absent, and wherein the amino acid sequence protects a plant cell against heat, and wherein the amino acid sequence encodes at least one nucleotide binding site. Applicants are also claiming a seed from a transformed plant.

Given the 112 second indefiniteness of "plant Hsp100 family amino acid sequence" as discussed above, the recitation "plant Hsp100 family amino acid sequence" is interpreted to mean any heat shock protein absent evidence to the contrary.

Malik et al teach carrot cells and plants transformed with a construct comprising an endogenous heat shock protein, Hsp17.7, operably linked to either the 35S promoter (page 97, 2nd paragraph under "Experimental procedures"). Malik et al present data that transformed plants comprising said construct are more thermotolerant than plants not comprising said

construct (page 92, Figure 4). Absent evidence to the contrary, it would be inherent that Hsp17.7 is necessary for cellular functioning when a heat stress is applied and is not necessary for cellular functioning when the stress is absent and the Hsp17.7 protein comprises at least one nucleotide binding site. Malik et al teach growing plants and collecting seed (page 97, right column, 3rd paragraph).

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

10. Claims 1-9, 12-16, 27-32, 34-42 are rejected under 35 U.S.C. 103(a) as being unpatentable over Malik et al (1999 The Plant Journal 20(1):89-99) in view of Schirmer et al (1994, The Plant Cell 6:1899-1909, listed in IDS).

The claims are drawn to a transgenic plant and method of increasing stress tolerance of a plant, wherein the stress is thermotolerance, comprising a construct comprising a promoter operably linked to a nucleic acid sequence encoding a plant Hsp100 family amino acid sequence, wherein said Hsp100 family amino acid sequence is SEQ ID NO:17, wherein said plant Hsp100 family amino acid sequence is endogenous to said transgenic plant, wherein said nucleic acid sequence encodes an amino acid sequence having at least about 60% overall amino acid homology to Arabidopsis Hsp101 amino acid sequence, wherein said amino acid sequence is a

functionally equivalent to an Hsp100 amino acid sequence or wherein said nucleic acid sequence has sequence similarity with SEQ ID NO:30, and wherein said transgenic plant is selected from the list of claim 6, and wherein said promoter is the 35S cauliflower mosaic virus promoter, and wherein said amino acid sequence protects the plant from more than one type of stress and is necessary for cellular functioning when a stress is present and is not necessary for cellular functioning when the stress is absent, and wherein the amino acid sequence protects a plant cell against heat, and wherein the amino acid sequence encodes at least one nucleotide binding site. The claims are also drawn to said method comprising seedlings, and a method of producing a crop comprising the above recited method and wherein a crop plant is selected from the plants listed in claim 16, and a seed of a transgenic plant,

The teachings of Malik et al have been discussed above.

Malik et al do not teach the Arabidopsis Hsp101 amino acid sequence.

Schirmer et al teach the Arabidopsis Hsp101 amino acid sequence. Given the indefiniteness of "Hsp100 family amino acid sequence" as stated above, given the lack of evidence to the contrary, the office interprets the Arabidopsis Hsp101 amino acid sequence to be a member of the Hsp100 family amino acid sequence and it is inherent that the Arabidopsis Hsp101 amino acid sequence comprises a nucleotide binding site.

Given the recognition of those of ordinary skill in the art the value of transforming a plant with a Hsp protein to increase thermotolerance as taught by Malik et al, it would have been obvious to utilize the methods of Malik et al and to incorporate the nucleic acid encoding the Arabidopsis Hsp101 amino acid sequence of Schirmer et al. Shirmer et al supply the motivation for incorporating said nucleic acid sequence by stating "Therefore, it may be possible to

manipulate expression of HSP100 proteins to engineer plants with greater stress tolerance" (page 1906, left column, last sentence of 1st full paragraph). Given the 112 2nd indefiniteness of "functionally equivalent" as stated above, the Office contends that the Hsp protein of Shirmer et al would inherently have the same function as an Hsp100 amino acid sequence. It would be a design chose to choose any of the plants listed in claim 6 or crop plants listed in claim 16.

11. Claims 1-6, 12-16, 27-32, and 34-42 are rejected under 35 U.S.C. 103(a) as being unpatentable over Harndahl et al (1998, Photosynthesis: Mechanisms and Effects, Proceedings of the International Congress on Photosynthesis, 11th, Budapest, Aug. 17-22, Volume 4, 2461-2464, Ed Garab, Gyozo. Kluwer Academic Publishers: Dordrecht, Neth.) in view of Schirmer et al (1994, The Plant Cell 6:1899-1909).

The claims are drawn to a transgenic plant and method of increasing stress tolerance of a plant, wherein the stress is thermotolerance, comprising a construct comprising a promoter operably linked to a nucleic acid sequence encoding a plant Hsp100 family amino acid sequence, wherein said Hsp100 family amino acid sequence is SEQ ID NO:17, wherein said plant Hsp100 family amino acid sequence is endogenous to said transgenic plant, wherein said nucleic acid sequence encodes an amino acid sequence having at least about 60% overall amino acid homology to Arabidopsis Hsp101 amino acid sequence, wherein said amino acid sequence is a functionally equivalent to an Hsp100 amino acid sequence or wherein said nucleic acid sequence has sequence similarity with SEQ ID NO:30, and wherein said transgenic plant is selected from the list of claim 6, and wherein said amino acid sequence protects the plant from more than one type of stress and is necessary for cellular functioning when a stress is present and is not

necessary for cellular functioning when the stress is absent, and wherein the amino acid sequence protects a plant cell against heat, and wherein the amino acid sequence encodes at least one nucleotide binding site. The claims are also drawn to said method comprising seedlings, and a method of producing a crop comprising the above recited method and wherein a crop plant is selected from the plants listed in claim 16, and a seed of a transgenic plant.

Given the 112 second indefiniteness of "plant Hsp100 family amino acid sequence" as discussed above, the recitation "plant Hsp100 family amino acid sequence" is interpreted to mean any heat shock protein absent evidence to the contrary.

Harndahl et al teach transgenic Arabidopsis plants which overexpress HSP21 are resistant to heat stress (abstract). The Office interprets Arabidopsis to be an ornamental plant and it would be inherent that seedlings have increased heat tolerance and seed would be collected. Absent evidence to the contrary, it would be inherent that HSP21 is necessary for cellular functioning when a heat stress is applied and is not necessary for cellular functioning when the stress is absent and the HSP21 protein comprises at least one nucleotide binding site.

Harndahl et al do not teach the Arabidopsis Hsp101 amino acid sequence.

Schirmer et al teach the Arabidopsis Hsp101 amino acid sequence. Given the indefiniteness of "Hsp100 family amino acid sequence" as stated above, given the lack of evidence to the contrary, the office interprets the Arabidopsis Hsp101 amino acid sequence to be a member of the Hsp100 family amino acid sequence and it is inherent that the Arabidopsis Hsp101 amino acid sequence comprises a nucleotide binding site.

Given the recognition of those of ordinary skill in the art the value of transforming a plant with a HSP protein to increase thermotolerance as taught by Harndahl et al, it would have been

obvious to utilize the methods of Harndahl et al and to incorporate the nucleic acid encoding the Arabidopsis Hsp101 amino acid sequence of Schirmer et al. Shirmer et al supply the motivation for incorporating said nucleic acid sequence by stating "Therefore, it may be possible to manipulate expression of HSP100 proteins to engineer plants with greater stress tolerance" (page 1906, left column, last sentence of 1st full paragraph). Given the 112 2nd indefiniteness of "functionally equivalent" as stated above, the Office contends that the Hsp protein of Shirmer et al would inherently have the same function as an Hsp100 amino acid sequence. It would be a design chose to choose any of the plants listed in claim 6 or crop plants listed in claim 16.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

12. Claims 27 and 28 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

Claims 27 and 28 are drawn to a seed of the transformed plant. Due to Mendelian inheritance of genes, a single gene introduced into a parent plant would only be transferred at most to half the male gametes and half the female gametes. This translates into only three quarters of the progeny having at least a single copy of the transgene and one quarter of the progeny would not carry a copy of the transgene. Given that there is no indication that there would be any other distinguishable characteristics of the claimed progeny (seeds), it is unclear whether the claimed seeds would be distinguishable from seeds that would occur in nature. See

Diamond v. Chakrabarty, 447 U.S. 303 (1980), *Funk Bros. Seed Co. v. Kalo Inoculant Co.*, 333 U.S. 127, 76 USPQ 280 (1948), and *In re Bergy , Coats, and Malik* 195 USPQ 344, (CCPA) 1977. The amendment of the claims to recite that the seeds comprise the construct that was introduced into the parent plant would overcome the rejection.

13. No claims are allowed.

14. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Stuart F. Baum whose telephone number is 571-272-0792. The examiner can normally be reached on M-F 8:30-5:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson can be reached on 571-272-0804. The fax phone number for the organization where this application or proceeding is assigned is (703) 872-9306.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 703-308-0196.

Stuart F. Baum Ph.D.
Patent Examiner
Art Unit 1638
March 19, 2004